

RAW SEQUENCE LISTING

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Application Serial Number: 10/537, 507 A
Source: IFWP
Date Processed by STIC: 08/03/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 08/03/2006

PATENT APPLICATION: US/10/537,507A

TIME: 09:36:16

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J537507A.raw

3 <110> APPLICANT: Aarhus Universitet
 5 <120> TITLE OF INVENTION: Method for determining predisposition to manifestation of
 immune system
 6 related diseases
 8 <130> FILE REFERENCE: P 706 DK 02
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/537,507A
 C--> 10 <141> CURRENT FILING DATE: 2005-06-03
 10 <160> NUMBER OF SEQ ID NOS: 8
 12 <170> SOFTWARE: PatentIn version 3.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 671
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Homo sapiens
 19 <400> SEQUENCE: 1
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 22 1 5 10 15
 25 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
 26 20 25 30
 29 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
 30 35 40 45
 33 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
 34 50 55 60
 37 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
 38 65 70 75 80
 41 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
 42 85 90 95
 45 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
 46 100 105 110
 49 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
 50 115 120 125
 53 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
 54 130 135 140
 57 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
 58 145 150 155 160
 61 Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
 62 165 170 175
 65 Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
 66 180 185 190
 69 Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
 70 195 200 205
 73 Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
 74 210 215 220
 77 Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
 78 225 230 235 240

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81 Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
82                245                250                255
85 Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
86                260                265                270
89 Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
90                275                280                285
93 Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
94                290                295                300
97 Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
98 305                310                315                320
101 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
102                325                330                335
105 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
106                340                345                350
109 Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
110                355                360                365
113 Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
114                370                375                380
117 Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
118 385                390                395                400
121 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
122                405                410                415
125 Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
126                420                425                430
129 Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
130                435                440                445
133 Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
134                450                455                460
137 Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
138 465                470                475                480
141 Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
142                485                490                495
145 Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
146                500                505                510
149 Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
150                515                520                525
153 Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
154                530                535                540
157 Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
158 545                550                555                560
161 Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
162                565                570                575
165 Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
166                580                585                590
169 Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
170                595                600                605
173 Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
174                610                615                620
177 Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp

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178 625          630          635          640
181 Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys
182          645          650          655
185 Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
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190 <211> LENGTH: 170
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
197 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
198 1          5          10          15
201 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
202          20          25          30
205 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
206          35          40          45
209 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
210          50          55          60
213 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
214 65          70          75          80
217 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
218          85          90          95
221 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
222          100          105          110
225 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
226          115          120          125
229 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
230          130          135          140
233 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
234 145          150          155          160
237 Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
238          165          170
241 <210> SEQ ID NO: 3
242 <211> LENGTH: 2061
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: cDNA encoding human MASP-2
249 <400> SEQUENCE: 3
250 atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttggggccc 60
252 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120
254 aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
256 ttcacccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240
258 tcggggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcggggc 300
260 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac 360
262 tactccaacg agaagccgtt cacgggggtt gaggccttct atgcagccga ggacattgac 420
264 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480
266 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc 540
268 tcagccctgt gctccggcca ggtcttcacc cagaggtctg gggagctcag cagccctgaa 600

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270 taccacacggc cgtatcccaa actctccagt tgcacttaca gcatcagcct ggaggagggg      660
272 ttcagtgtca ttctggactt tgtggagtc ttcgatgtgg agacacaccc tgaaaccctg      720
274 tgtccctacg actttctcaa gattcaaaca gacagagaag aacatggccc attctgtggg      780
276 aagacattgc cccacaggat tgaaacaaaa agcaacacgg tgaccatcac ctttgtcaca      840
278 gatgaatcag gagaccacac aggctggaag atccactaca cgagcacagc gcagccttgc      900
280 ccttatccga tggcgccacc taatggccac gtttcacctg tgcaagccaa atacatcctg      960
282 aaagacagct tctccatctt ttgcgagact ggctatgagc ttctgcaagg tcaattgccc     1020
284 ctgaaatcct ttactgcagt ttgtcagaaa gatggatctt gggaccggcc aatgcccgcg     1080
286 tgcagcattg ttgactgtgg cctcctgat gatctacca gtggccgagt ggagtacatc     1140
288 acaggctctg gagtgaccac ctacaaagct gtgattcagt acagctgtga agagaccttc     1200
290 tacacaatga aagtgaatga tggtaaatat gtgtgtgagg ctgatggatt ctggacgagc     1260
292 tccaaaggag aaaaatcact cccagtctgt gagcctgttt gtggactatc agcccgacaca     1320
294 acaggagggc gtatatatgg agggcaaaaag gcaaaacctg gtgattttcc ttggcaagtc     1380
296 ctgatattag gtggaaccac agcagcaggt gcacttttat atgacaactg ggtcctaaca     1440
298 gctgctcatg ccgtctatga gcaaaaaacat gatgcatccg ccttgacat tcgaatgggc     1500
300 accctgaaaa gactatcacc tcattataca caagcctggt ctgaagctgt ttttatacat     1560
302 gaaggttata ctcatgatgc tggctttgac aatgacatag cactgattaa attgaataac     1620
304 aaagttgtaa tcaatagcaa catcacgcct atttgtctgc caagaaaaga agctgaatcc     1680
306 tttatgagga cagatgacat tggaaactgca tctggatggg gattaaccca aaggggtttt     1740
308 cttgctagaa atctaagtta tgtcgacata ccgattgttg accatcaaaa atgtactgct     1800
310 gcatatgaaa agccacccta tccaagggga agtgtaaact ctaacatgct ttgtgctggc     1860
312 ttagaaagtg ggggcaagga cagctgcaga ggtgacagcg gaggggcact ggtgtttcta     1920
314 gatagtgaaa cagagagggt gtttgtggga ggaatagtgt cctgggggttc catgaattgt     1980
316 ggggaagcag gtcagtatgg agtctacaca aaagttatta actatatccc ctggatcgag     2040
318 aacataatta gtgattttta a                                     2061
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 558
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: cDNA encoding human MAP-19
329 <400> SEQUENCE: 4
330 atgaggctgc tgacctctct gggccttctg tgtggctcgg tggccacccc cttgggcccg      60
332 aagtggcctg aacctgtggt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc     120
334 aatgaccagg agcggcgctg gacctgact gcaccccccg gctaccgcct gcgcctctac     180
336 ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc     240
338 tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcggggc     300
340 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac     360
342 tactccaacg agaagccgtt cacgggggttc gaggccttct atgcagccga ggacattgac     420
344 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg     480
346 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc     540
348 tcagagcaga gcctctag                                     558
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 21
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: upper PCR primer
359 <400> SEQUENCE: 5

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360 gcgagtacga cttcgtcaag g 21
363 <210> SEQ ID NO: 6
364 <211> LENGTH: 21
365 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: lower PCR primer
371 <400> SEQUENCE: 6
372 ctcggctgca tagaaggcct c 21
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
378 <213> ORGANISM: Artificial Sequence
380 <220> FEATURE:
381 <223> OTHER INFORMATION: upper PCR primer
383 <400> SEQUENCE: 7
384 ccagaccttt ggaaagttag c 21
387 <210> SEQ ID NO: 8
388 <211> LENGTH: 21
389 <212> TYPE: DNA
390 <213> ORGANISM: Artificial Sequence
392 <220> FEATURE:
393 <223> OTHER INFORMATION: lower PCR primer
395 <400> SEQUENCE: 8
396 ggctcaagtt ccaagtattg c 21
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VERIFICATION SUMMARY

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Output Set: N:\CRF4\08032006\J537507A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date